In the Specification:

Please amend the specification as shown:

Please delete paragraph [0010] on and replace it with the following paragraph:

[0010] The present invention also provides a humanized MN3 (hMN3) monoclonal antibody (MAb) or fragment thereof comprising one or more complementarity-determining regions (CDRs) of a murine MN3 MAb and one or more framework (FR) regions of the light and heavy chain variable regions of a human antibody and the light and heavy chain constant regions of a human antibody. The CDRs of the light chain variable region of the humanized can be selected from a MN3 MAb CDR1 comprising amino acids RSSQSIVHSNGNTYLE **(SEQ ID NO: 1)**; a CDR2 comprising an amino acid sequence of KVSNRFS **(SEQ ID NO: 2)**; and a CDR3 comprising an amino acid sequence of FQGSHVPPT **(SEQ ID NO: 3)**. The CDRs of the heavy chain variable region of the MN3 MAb can be selected from a CDR1 comprising amino acids NYGMN **(SEQ ID NO: 4)**; a CDR2 comprising amino acids WINTYTGEPTYADDFKG **(SEQ ID NO: 5)**; and a CDR3 comprising amino acids KGWMDFNGSSLDY **(SEQ ID NO: 6)**.

Please delete paragraph [0013] on and replace it with the following paragraph:

[0013] Also provided by the present invention is a CDR-grafted humanized heavy chain comprising the complementarity determining regions (CDRs) of a murine MN3 MAb and the framework region of the heavy chain variable region of a human antibody and the heavy chain constant region of a human antibody, wherein the CDRs of the heavy chain variable region of the humanized MN3 MAb comprises CDR1 comprising an amino acid sequence of NYGMN **(SEQ ID NO: 4)**; CDR2 comprising an amino acid sequence of

WINTYTGEPTYADDFKG **(SEQ ID NO: 5)** and CDR3 comprising an amino acid sequence of KGWMDFNGSSLDY **(SEQ ID NO: 6)**.

Please delete paragraph [0014] on and replace it with the following paragraph:

[0014] A CDR-grafted humanized light chain comprising the complementarity determining regions (CDRs) of a murine MN3 MAb and the framework region of the light chain variable region of a human antibody and the light chain constant region of a human antibody, wherein the CDRs of the light chain variable region of the humanized MN3 MAb comprises CDR1 comprising an amino acid sequence of RSSQSIVHSNGNTYLE **(SEQ ID NO: 1)**; CDR2 comprising an amino acid sequence of KVSNRFS **(SEQ ID NO: 2)** and CDR3 comprising an amino acid sequence of FQGSHVPPT **(SEQ ID NO: 3)**.

Please delete paragraph [0019] on and replace it with the following paragraph:

[0019] Further provided is a chimeric MN3 (cMN3) monoclonal antibody, or fragment thereof comprising the complementarity-determining regions (CDRs) of a murine MN3 MAb and the framework (FR) regions of the light and heavy chain variable regions of said murine anti-CD 20 MAb and the light and heavy chain constant regions of a human antibody, wherein the CDRs of the light chain variable region of the chimeric MN3 MAb comprises CDR1 comprising an amino acid sequence RSSQSIVHSNGNTYLE **(SEQ ID NO: 1)**; CDR2 comprising an amino acid sequence of KVSNRFS; and CDR3 comprise an amino acid sequence of FQGSHVPPT **(SEQ ID NO: 2)**; and the CDRs of the heavy chain variable region of the MN3 MAb comprise CDR1 comprising amino acids NYGMN **(SEQ ID NO: 4)**; CDR2 comprising amino acids WINTYTGEPTYADDFKG **(SEQ ID NO: 5)** and CDR3 comprising amino acids KGWMDFNGSSLDY **(SEQ ID NO: 6)**.

Please delete paragraph [0021] on and replace it with the following paragraph:

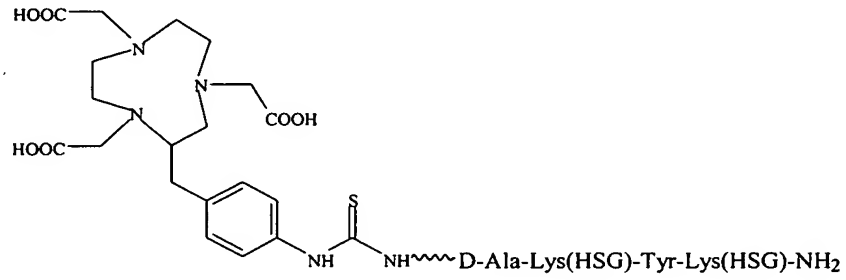
[0021] The invention also provides a human MN3 (MN3) monoclonal antibody (MAb) or fragment thereof comprising the light and heavy chain variable and constant regions of a human antibody, wherein the CDRs of the light chain variable region of the human MN3 MAb comprises comprises CDR1 comprising an amino acid sequence RSSQSIVHSNGNTYLE **(SEQ ID NO: 1)**; CDR2 comprising an amino acid sequence of KVSNRFS **(SEQ ID NO: 2)**; and CDR3 comprise an amino acid sequence of FQGSHVPPT **(SEQ ID NO: 3)**; and the CDRs of the heavy chain variable region of the MN3 MAb comprise CDR1 comprising amino acids NYGMN **(SEQ ID NO: 4)**; CDR2 comprising amino acids WINTYTGEPTYADDFKG **(SEQ ID NO: 5)** and CDR3 comprising amino acids KGWMDFNGSSLDY **(SEQ ID NO: 6)**.

Please delete paragraph [0049] on and replace it with the following paragraph:

[0049] Considered herein is a method for detecting or treating tumors or ischemic lesions expressing an antigen recognized by an anti-granulocyte MAb in a mammal, comprising: (A) administering an effective amount of a bispecific antibody or antibody fragment comprising at least one arm that specifically binds a targeted tissue and at least one other arm that specifically binds a targetable conjugate, wherein said one arm that specifically binds a targeted tissue is an anti-granulocyte antibody or fragment thereof; and (B) administering a targetable conjugate. The targetable conjugate can be selected from the group consisting of (i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2; (ii) DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2 **(SEQ ID NO: 7)**; (iii) Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH_2; (iv) DOTA-D-Asp-D-Lys(HSG)-D-Asp-D-Lys(HSG)- NH_2; (v) DOTA-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vi) DOTA-D-Tyr-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vii) DOTA-D-Ala-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (viii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-NH_2; (ix) Ac-D-Phe-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-NH_2; (x) Ac-D-Phe-

D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xi) Ac-D-Phe-D-Lys(Bz-DTPA)-D-Tyr-D-Lys(Bz-DTPA)-NH_2; (xii) Ac-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiv) (Tscg-Cys)-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(DOTA)-NH_2; (xv) Tscg-D-Cys-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvi) (Tscg-Cys)-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvii) Ac-D-Cys-D-Lys(DOTA)-D-Tyr-D-Ala-D-Lys(DOTA)-D-Cys-NH_2; (xviii) Ac-D-Cys-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xix)Ac-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-D-Lys(TscG-Cys)-NH_2; (xx) Ac-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-D-Lys(TscG-Cys)-NH_2;

(xxi)



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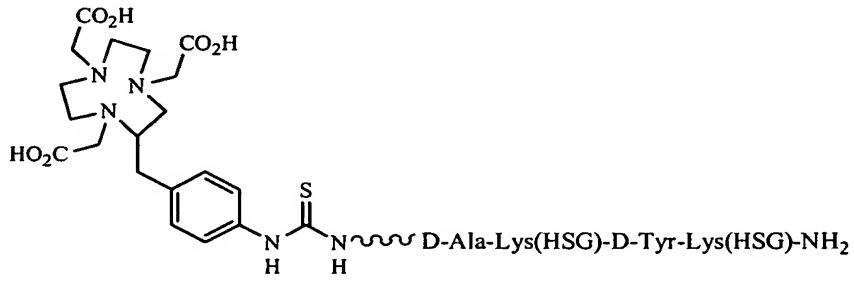
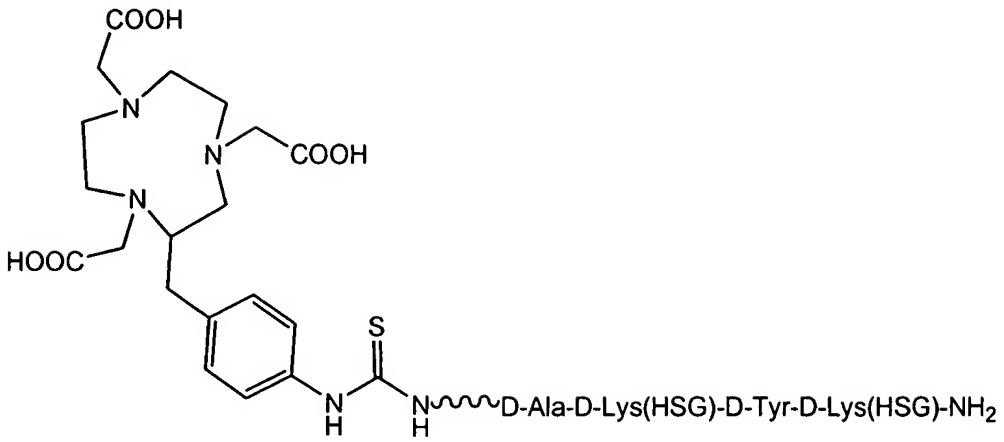


(xxiii) 

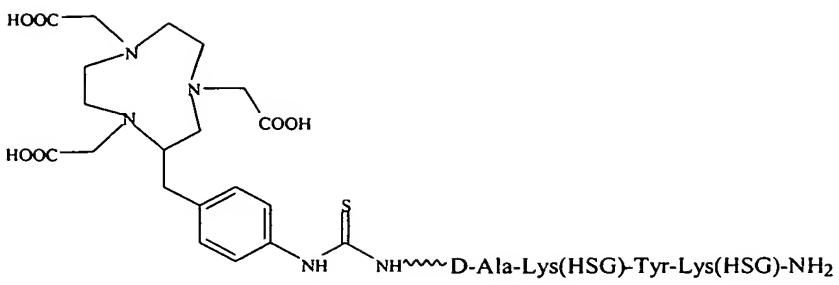
Additional targetable conjugates that can be used with the present methods include those disclosed in U.S. Patent Application No. 60/478,403.

Please delete paragraph [0051] on and replace it with the following paragraph:

[0051] Also contemplated herein is a kit useful for treating or identifying diseased tissues involving accumulation of normal or malignant granuloctes in a subject comprising: (A) a bi-specific antibody or antibody fragment having at least one arm that specifically binds a targeted tissue and at least one other arm that specifically binds a targetable conjugate, wherein said one arm that specifically binds a targeted tissue is an anti-granulocyte antibody or fragment thereof; (B) a first targetable conjugate which comprises a carrier portion which comprises or bears at least one epitope recognizable by said at least one other arm of said bi-specific antibody or antibody fragment, and one or more conjugated therapeutic or diagnostic agents; and (C) optionally, a clearing composition useful for clearing non-localized antibodies and antibody fragments; and (D) optionally, when said therapeutic agent conjugated to said first targetable conjugate is an enzyme, (i) a prodrug, when said enzyme is capable of converting said prodrug to a drug at the target site; or (ii) a drug which is capable of being detoxified in said subject to form an intermediate of lower toxicity, when

said enzyme is capable of reconverting said detoxified intermediate to a toxic form, and, therefore, of increasing the toxicity of said drug at the target site, or (iii) a prodrug which is activated in said subject through natural processes and is subject to detoxification by conversion to an intermediate of lower toxicity, when said enzyme is capable of reconverting said detoxified intermediate to a toxic form, and, therefore, of increasing the toxicity of said drug at the target site, or (iv) a second targetable conjugate which comprises a carrier portion which comprises or bears at least one epitope recognizable by said at least one other arm of said bi-specific antibody or antibody fragment, and a prodrug, when said enzyme is capable of converting said prodrug to a drug at the target site. Preferably, the targetable conjugate is selected from the group consisting of:

(i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2; (ii) DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2; **(SEQ ID NO: 7)** (iii) Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH_2; (iv) DOTA-D-Asp-D-Lys(HSG)-D-Asp-D-Lys(HSG)- NH_2; (v) DOTA-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vi) DOTA-D-Tyr-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vii) DOTA-D-Ala-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (viii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-NH_2; (ix) Ac-D-Phe-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-NH_2; (x) Ac-D-Phe-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xi) Ac-D-Phe-D-Lys(Bz-DTPA)-D-Tyr-D-Lys(Bz-DTPA)-NH_2; (xii) Ac-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiv) (Tscg-Cys)-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(DOTA)-NH_2; (xv) Tscg-D-Cys-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvi) (Tscg-Cys)-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvii) Ac-D-Cys-D-Lys(DOTA)-D-Tyr-D-Ala-D-Lys(DOTA)-D-Cys-NH_2; (xviii) Ac-D-Cys-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xix)Ac-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-D-Lys(TscG-Cys)-NH_2; (xx) Ac-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-D-Lys(TscG-Cys)-NH_2;

(xxi) 

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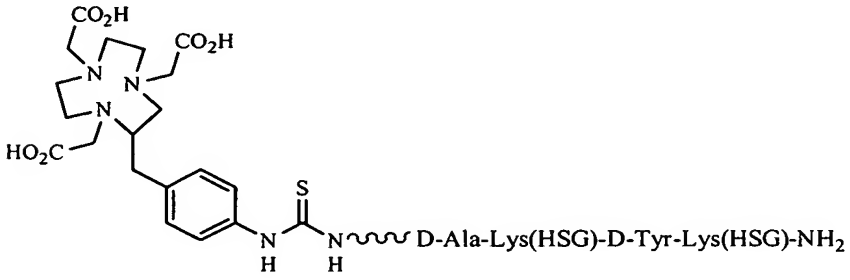
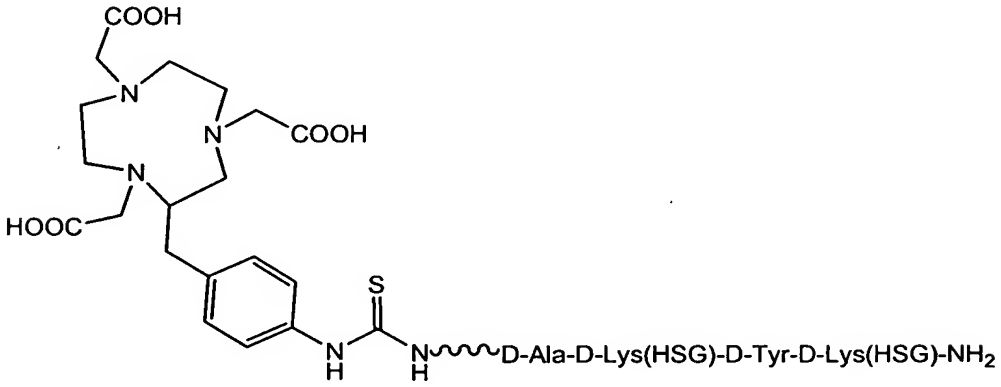
(xxii) 

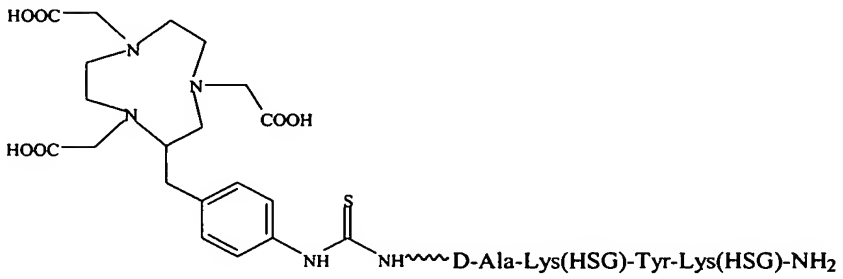
(xxiii) 

Please delete paragraph [0053] on and replace it with the following paragraph:

[0053] Another embodiment is a method for imaging malignant or ischemic tissue or cells in a mammal expressing an antigen recognized by an anti-granulocyte MAb, comprising: (A) administering an effective amount of a bispecific antibody or antibody fragment comprising at least one arm that specifically binds a marker associated with a targeted tissue and at least one other arm that specifically binds a targetable conjugate, wherein said

marker is an antigen recognized by the anti-granulocyte MAb; and (B) administering a targetable conjugate selected from the group consisting of

(i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2; (ii) DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2; **(SEQ ID NO: 7)** (iii) Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH_2; (iv) DOTA-D-Asp-D-Lys(HSG)-D-Asp-D-Lys(HSG)- NH_2; (v) DOTA-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vi) DOTA-D-Tyr-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vii) DOTA-D-Ala-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (viii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-NH_2; (ix) Ac-D-Phe-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-NH_2; (x) Ac-D-Phe-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xi) Ac-D-Phe-D-Lys(Bz-DTPA)-D-Tyr-D-Lys(Bz-DTPA)-NH_2; (xii) Ac-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiv) (Tscg-Cys)-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(DOTA)-NH_2; (xv) Tscg-D-Cys-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvi) (Tscg-Cys)-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvii) Ac-D-Cys-D-Lys(DOTA)-D-Tyr-D-Ala-D-Lys(DOTA)-D-Cys-NH_2; (xviii) Ac-D-Cys-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xix)Ac-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-D-Lys(TscG-Cys)-NH_2; (xx) Ac-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-D-Lys(TscG-Cys)-NH_2;

(xxi) 

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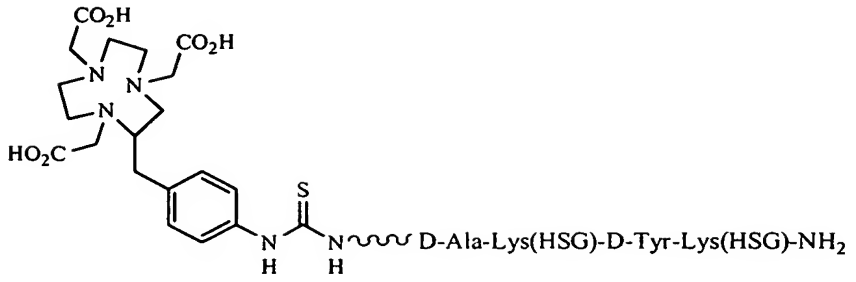
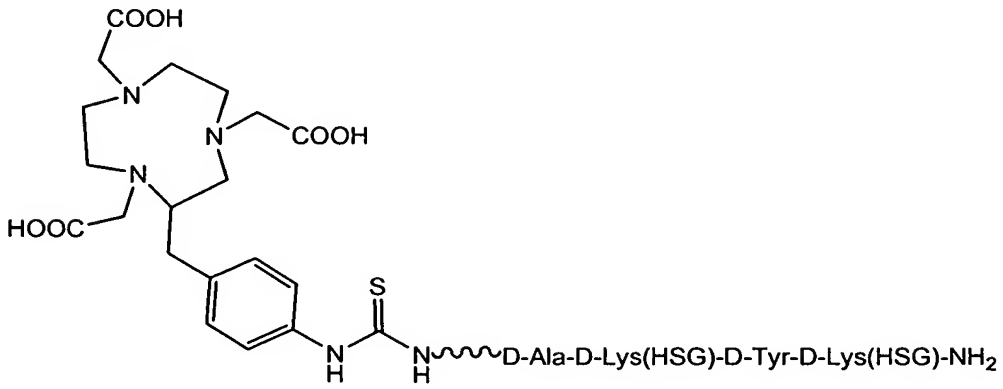
(xxii) 

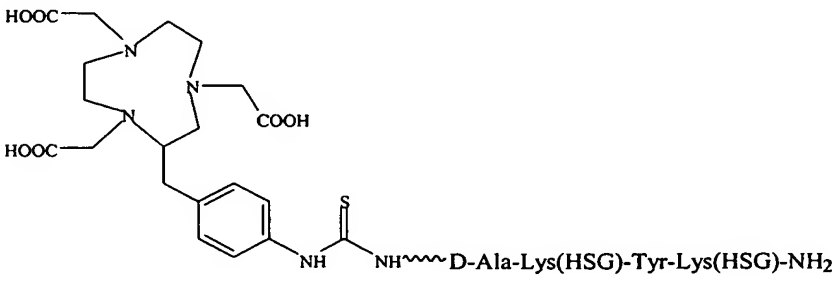
(xxiii) 

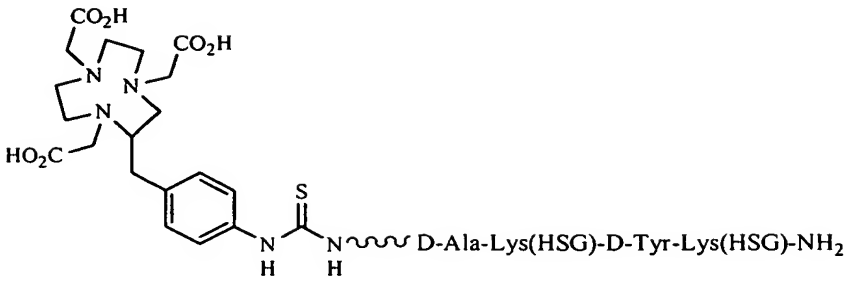
Please delete paragraph [0054] on and replace it with the following paragraph:

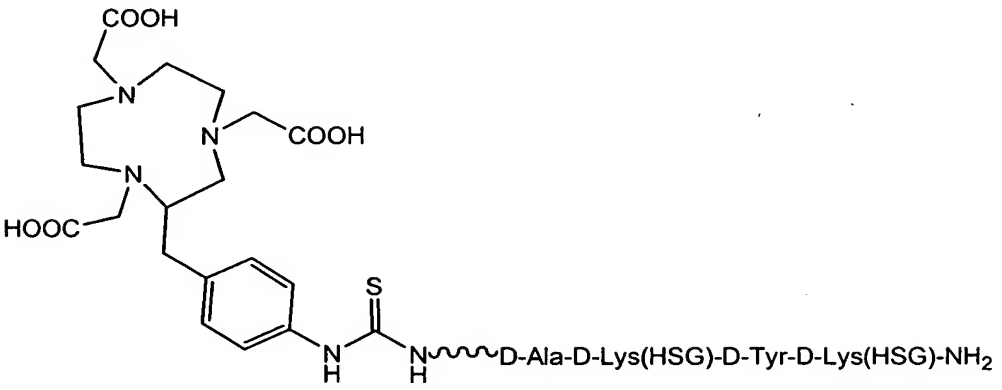
[0054] The invention also contemplates a method of intraoperatively identifying/disclosing diseased tissues expressing an antigen recognized by an anti-granulocyte MAb, in a subject, comprising: (A) administering an effective amount of a bispecific antibody or antibody fragment comprising at least one arm that specifically binds an antigen recognized by the anti-granulocyte MAb and at least one other arm that specifically binds a targetable conjugate, wherein said one arm that specifically binds a targeted tissue is an anti-granulocyte MAb antibody or fragment thereof; and (B) administering a targetable conjugate selected from the group consisting of

(i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2; (ii) DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2; **(SEQ ID NO: 7)** (iii) Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH_2; (iv) DOTA-D-Asp-D-Lys(HSG)-D-Asp-D-Lys(HSG)- NH_2; (v) DOTA-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vi) DOTA-D-Tyr-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vii) DOTA-D-Ala-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (viii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-NH_2; (ix) Ac-D-Phe-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-NH_2; (x) Ac-D-Phe-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xi) Ac-D-Phe-D-Lys(Bz-DTPA)-D-Tyr-D-Lys(Bz-DTPA)-NH_2; (xii) Ac-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiv) (Tscg-Cys)-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(DOTA)-NH_2; (xv) Tscg-D-Cys-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvi) (Tscg-Cys)-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvii) Ac-D-Cys-D-Lys(DOTA)-D-Tyr-D-Ala-D-Lys(DOTA)-D-Cys-NH_2; (xviii) Ac-D-Cys-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xix)Ac-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-D-Lys(TscG-Cys)-NH_2; (xx) Ac-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-D-Lys(TscG-Cys)-NH_2;

(xxi)



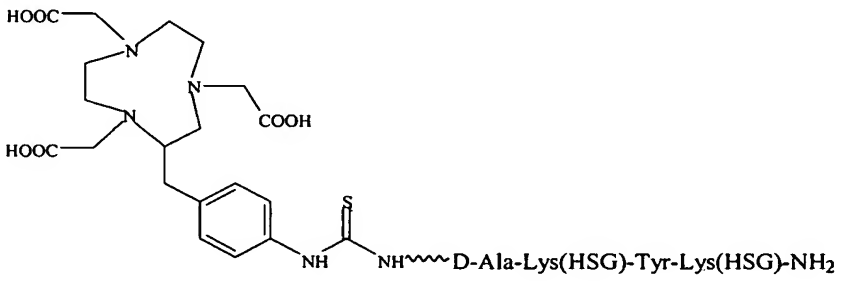
(xxii) 

(xxiii) 

Please delete paragraph [0055] on and replace it with the following paragraph:

[0055] Also described herein is a method for the endoscopic identification of diseased tissues expressing an antigen recognized by an anti-granulocyte MAb, in a subject, comprising: (A) administering an effective amount of a bispecific antibody or antibody fragment comprising at least one arm that specifically binds an antigen recognized by an anti-granulocyte MAb and at least one other arm that specifically binds a targetable conjugate wherein said one arm that specifically binds a targeted tissue is a MN3 antibody or fragment thereof; and (B) administering a targetable conjugate selected from the group consisting of

(i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2; (ii) DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2; **(SEQ ID NO: 7)** (iii) Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH_2; (iv) DOTA-D-Asp-D-Lys(HSG)-D-Asp-D-Lys(HSG)- NH_2; (v) DOTA-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vi) DOTA-D-Tyr-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vii) DOTA-D-Ala-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (viii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-NH_2; (ix) Ac-D-Phe-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-NH_2; (x) Ac-D-Phe-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xi) Ac-D-Phe-D-Lys(Bz-DTPA)-D-Tyr-D-Lys(Bz-DTPA)-NH_2; (xii) Ac-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiv) (Tscg-Cys)-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(DOTA)-NH_2; (xv) Tscg-D-Cys-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvi) (Tscg-Cys)-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvii) Ac-D-Cys-D-Lys(DOTA)-D-Tyr-D-Ala-D-Lys(DOTA)-D-Cys-NH_2; (xviii) Ac-D-Cys-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xix)Ac-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-D-Lys(TscG-Cys)-NH_2; (xx) Ac-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-D-Lys(TscG-Cys)-NH_2;

(xxi) 

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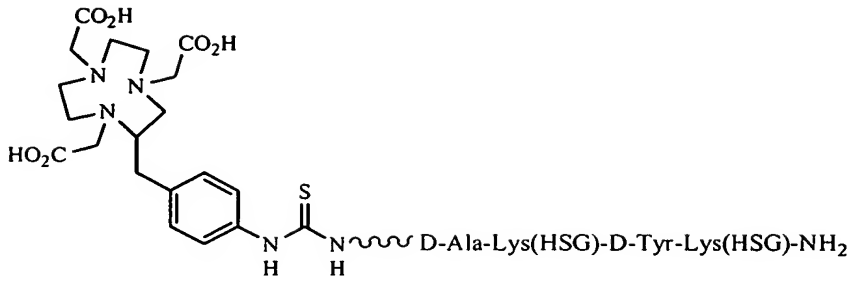

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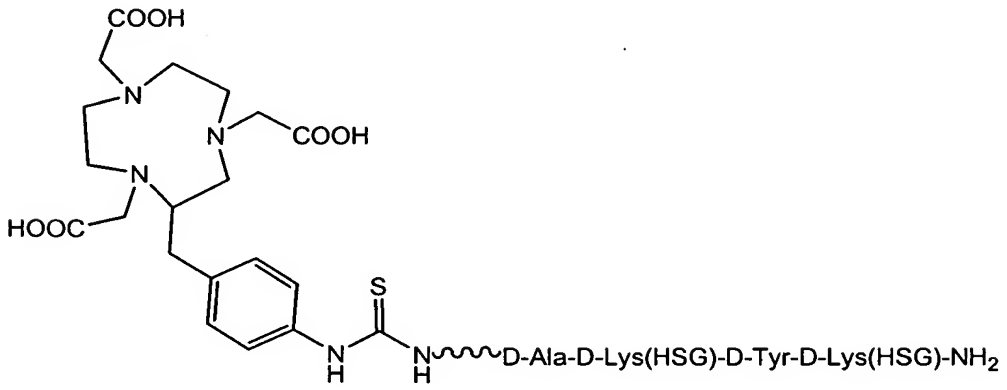
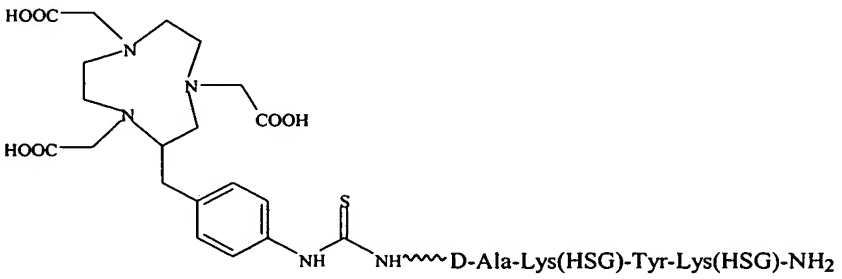


Please delete paragraph [0056] on and replace it with the following paragraph:

[0056] Another embodiment is a method for the intravascular identification of diseased tissues expressing an antigen recognized by an anti-granulocyte MAb, in a subject, comprising: (A) administering an effective amount of a bispecific antibody or antibody fragment comprising at least one arm that specifically binds an antigen recognized by the anti-granulocyte MAb and at least one other arm that specifically binds a targetable conjugate wherein said one arm that specifically binds a targeted tissue is a MN3 antibody or fragment thereof; and (B) administering a targetable conjugate selected from the group consisting of

(i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2; (ii) DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2; **(SEQ ID NO: 7)** (iii) Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH_2; (iv) DOTA-D-Asp-D-Lys(HSG)-D-Asp-D-Lys(HSG)- NH_2; (v) DOTA-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vi) DOTA-D-Tyr-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (vii) DOTA-D-Ala-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (viii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-NH_2; (ix) Ac-D-Phe-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-NH_2; (x) Ac-D-Phe-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xi) Ac-D-Phe-D-Lys(Bz-DTPA)-D-Tyr-D-Lys(Bz-DTPA)-NH_2; (xii) Ac-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiii) DOTA-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(Tscg-Cys)-NH_2; (xiv) (Tscg-Cys)-D-Phe-D-Lys(HSG)-D-Tyr-D-Lys(HSG)-D-Lys(DOTA)-NH_2; (xv) Tscg-D-Cys-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvi) (Tscg-Cys)-D-Glu-D-Lys(HSG)-D-Glu-D-Lys(HSG)-NH_2; (xvii) Ac-D-Cys-D-Lys(DOTA)-D-Tyr-D-Ala-D-Lys(DOTA)-D-Cys-NH_2; (xviii) Ac-D-Cys-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-NH_2; (xix)Ac-D-Lys(DTPA)-D-Tyr-D-Lys(DTPA)-D-Lys(TscG-Cys)-NH_2; (xx) Ac-D-Lys(DOTA)-D-Tyr-D-Lys(DOTA)-D-Lys(TscG-Cys)-NH_2;

(xxi) 

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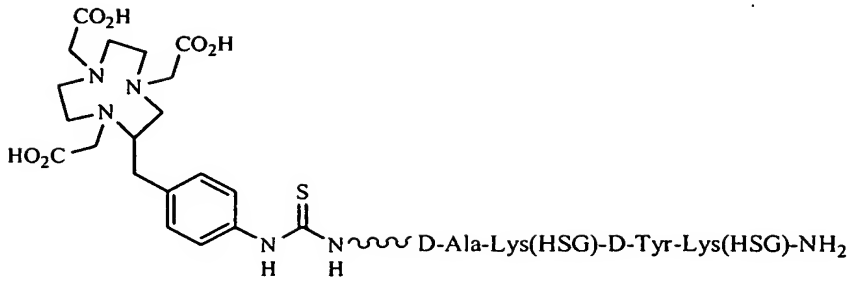

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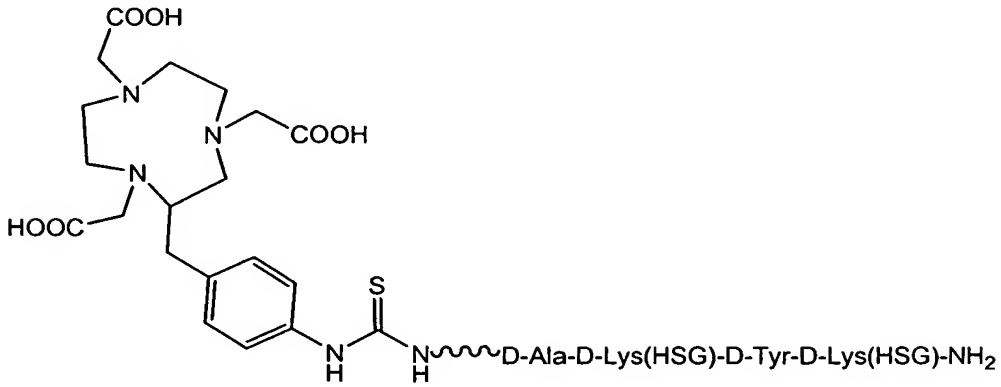


Please delete paragraph [0059] on and replace it with the following paragraph:

[0059] Figure 1 shows the cloned V_H and $V\kappa$ gene sequences of the murine MN3 by RT-PCR and the deduced amino acid sequences. Underlined arrows at 5'- and 3'-ends indicate the sequence of PCR primers used in cloning. Figure 1A shows the DNA **(SEQ ID NO: 8)** and amino acid **(SEQ ID NO: 9)** sequences of the MN3Vκ. Figure 1B shows the DNA **(SEQ ID NO: 10)** and amino acid **(SEQ ID NO: 11)** sequences of the MN3V_H. Amino acid sequences encoded by the corresponding DNA sequences are given as one letter codes below the nucleotide sequence. Numbering of the nucleotide sequence is on the right side. The amino acid residues in the putative CDR regions are shown in bold and underlined. Kabat's Ig molecule numbering is used for amino acid residues as shown by the numbering above the amino acid residues. The residues numbered by a letter following digits indicate

the insertion residues defined by Kabat numbering scheme. The insertion residues numbered with a letter only have the same preceeding digits as the previous one. For example, residues 27A, 27B, 27C, 27D, and 27E in Figure 1A are indicated as 82, A, B, and C27A, B, C, D, and E, respectively.

Please delete paragraph [0060] on and replace it with the following paragraph:

[0060] Figure 2 shows the DNA and amino acid sequences of the chimeric MN3 (cMN3) heavy and light chain variable regions. Figure 2A shows the DNA **(SEQ ID NO: 12)** and amino acid **(SEQ ID NO: 13)** sequences of the cMN3Vκ. Figure 2B shows the DNA **(SEQ ID NO: 14)** and amino acid **(SEQ ID NO: 15)** sequences of the cMN3VH. Amino acid sequences encoded by the corresponding DNA sequences are given as one letter codes. The amino acid residues in the CDR regions are shown in bold and underlined. Numbering of the nucleotide sequence is on the right side. The numbering of amino acids is same as that in Figure 1.

Please delete paragraph [0062] on and replace it with the following paragraph:

[0062] Figure 4 shows the alignment of the amino acid sequences of light and heavy chain variable regions of certain human antibodies, MN3 and hMN3. Figure 4A compares the amino acid sequences of the REI **(SEQ ID NO:16)**, MN3 **(SEQ ID NO:17)** and hMN3 **(SEQ ID NO:18)** light chain variable domains. Figure 4B is the amino acid sequence alignment of EU (FR1-3) **(SEQ ID NO:19)** and KOL (FR4) **(SEQ ID NO:22)**, MN3 **(SEQ ID NO:20)** and hMN3 **(SEQ ID NO:21)** heavy chain variable domains. Boxed regions represent the CDR regions. Dots indicate the residues in MN3 and hMN3 which are identical to the corresponding residues in REI V_K. Dashes represent gaps introduced to aid the alignment.

Both N- and C-terminal residues (underlined) of hMN3 are fixed by the staging vector used. The corresponding terminal residues of MN3 are not compared with that of the human sequences. Kabat's Ig molecule numbering scheme is used (same as in Figs. 1A and 1B, respectively).

Please delete paragraph [0063] on and replace it with the following paragraph:

[0063] Figure 5 discloses the nucleotide sequences of hMN3Vκ **(SEQ ID NO: 23)** and the adjacent flanking regions of the light chain staging vector, VKpBR2 **(SEQ ID NO: 24)** (Figure 5A) and hMN3VH **(SEQ ID NO: 25)** and the adjacent flanking regions of the heavy chain staging vector, VKpBS2 **(SEQ ID NO: 26)** (Figure 5B). The encoded amino acid sequences are shown as one letter codes below the corresponding DNA sequences. The non-translated nucleotide sequences are shown in lowercase. The restriction sites used for subcloning are underlined and indicated. The secretion signal peptide sequence is indicated by a double underline. Numbering of Vk and VH amino acid residues is the same as that in Figure 2.

Please delete paragraph [0076] on and replace it with the following paragraph:

[0076] In a preferred embodiment, the humanized MN3 MAb or fragment thereof of the present invention comprises the CDRs of a murine MN3 MAb and the framework (FR) regions of the light and heavy chain variable regions of a human antibody and the light and heavy chain constant regions of a human antibody. Preferably, the CDRs of the light chain variable region of the humanized MN3 MAb comprise a CDR1 that comprises an amino acid sequence of RSSQSIVHSNGNTYLE **(SEQ ID NO: 1)**, CDR2 that comprises an amino acid sequence of KVSNRFS **(SEQ ID NO: 2)**, and/or CDR3 that comprises an amino acid sequence of FQGSHVPPT **(SEQ ID NO: 3)**; and the CDRs of the heavy chain variable region

of the MN3 MAb comprise a CDR1 that comprises an amino acid sequence of NYGMN **(SEQ ID NO: 4)**, a CDR2 that comprises an amino acid sequence of WINTYTGEPTYADDFKG **(SEQ ID NO: 5)**, and/or a CDR3 that comprises an amino acid sequence of KGWMDFNGSSLDY **(SEQ ID NO: 6)**.

Please delete paragraph [0078] on and replace it with the following paragraph:

[0078] In a related vein, chimeric MN3 (cMN3) MAb or fragment thereof of the present invention comprises the CDRs of a murine MN3 MAb and the FR regions of the light and heavy chain variable regions of the murine MN3 MAb. In other words, the cMN3 antibody comprises the Fvs of the parental murine (i.e., mMN3) MAb, and the light and heavy chain constant regions of a human antibody, wherein the CDRs of the light chain variable region of the chimeric MN3 MAb comprise a CDR1 that comprises an amino acid sequence of RSSQSIVHSNGNTYLE **(SEQ ID NO: 1)**, CDR2 that comprises an amino acid sequence of KVSNRFS **(SEQ ID NO: 2)**, and/or CDR3 that comprises an amino acid sequence of FQGSHVPPT **(SEQ ID NO: 3)**; and the CDRs of the heavy chain variable region of the MN3 MAb comprise a CDR1 that comprises an amino acid sequence of NYGMN **(SEQ ID NO: 4)**, a CDR2 that comprises an amino acid sequence of WINTYTGEPTYADDFKG **(SEQ ID NO: 5)**, and/or a CDR3 that comprises an amino acid sequence of KGWMDFNGSSLDY **(SEQ ID NO: 6)**.

Please delete paragraph [0115] on and replace it with the following paragraph:

[00115] As used herein, the term antibody fusion protein is a recombinantly produced antigen-binding molecule in which two or more of the same or different natural antibody, single-chain antibody or antibody fragment segments with the same or different specificities are linked. An MN3 fusion protein comprises a binding site for an antigen recognized by MN3. The MN3 fusion protein and fragment thereof of the present invention comprise at least one arm that binds to the same epitope an antibody or antibody fragment comprising CDR1 of a heavy chain variable region that comprises an amino acid sequence of NYGMN **(SEQ ID NO: 4)**, a CDR2 that comprises an amino acid sequence of WINTYTGEPTYADDFKG **(SEQ ID NO: 5)**, and/or a CDR3 that comprises an amino acid sequence of KGWMDFNGSSLDY **(SEQ ID NO: 6)**, and/or CDR1 of a light chain variable region that comprises an amino acid sequence of RSSQSIVHSNGNTYLE **(SEQ ID NO: 1)**, CDR2 that comprises an amino acid sequence of KVSNRFS **(SEQ ID NO: 2)**, and/or CDR3 that comprises an amino acid sequence of FQGSHVPPT **(SEQ ID NO: 3)**.

Please delete paragraph [0133] on and replace it with the following paragraph:

[00133] Bispecific fusion proteins linking two or more different single-chain antibodies or antibody fragments are produced in similar manner. Recombinant methods can be used to produce a variety of fusion proteins. For example a fusion protein comprising a Fab fragment derived from a humanized monoclonal MN3 antibody and a scFv derived from a murine anti-diDTPA can be produced. A flexible linker, such as GGGS **(SEQ ID NO: 27)** connects the scFv to the constant region of the heavy chain of the MN3 antibody. Alternatively, the scFv can be connected to the constant region of the light chain of another humanized antibody. Appropriate linker sequences necessary for the in-frame connection of the heavy chain Fd to the scFv are introduced into the VL and VK domains through PCR reactions. The DNA fragment encoding the scFv is then ligated into a staging vector

containing a DNA sequence encoding the CH1 domain. The resulting scFv-CH1 construct is excised and ligated into a vector containing a DNA sequence encoding the VH region of an MN3 antibody. The resulting vector can be used to transfect an appropriate host cell, such as a mammalian cell for the expression of the bispecific fusion protein.

Please delete paragraph [0136] on and replace it with the following paragraph:

[00136] PCR cloning techniques are well-known in the art. In brief, however, PCR cloning of V_K and V_H gene fragments may be accomplished as follows. Total RNA may be isolated from a MN3 hybridoma cell line using commercially available kits such as the Fast Track RNA Isolation kit (Invitrogen, San Diego, CA). The first strand cDNA may then be reverse transcribed from RNA using a cDNA cycle kit (Invitrogen). In this process, 5 μg of total RNA is annealed to an oligo dT or random hexamer primer, or a murine IgG CH1-specific primer or a murine C_K-specific primer. Examples of such primers include CH1B (5' – ACA GTC ACT GAG CTG G – 3') **(SEQ ID NO: 28)** and CK3-BH1 (5' – GCC GGA TCC TGA CTG GAT GGT GGG AAG ATG GAT ACA – 3') **(SEQ ID NO: 29)**, respectively. The first strand cDNA may be used as templates to amplify the V_H and V_K sequences by PCR, as described by Orlandi *et al.* For the VK region, a primer pair such as VK1BACK (5' – GAC ATT CAG CTG ACC CAG TCT CCA – 3') **(SEQ ID NO: 30)** and IgKC3' (5' – CTC ACT GGA TGG TGG GAA GAT GGA TAC AGT TGG – 3') **(SEQ ID NO: 31)** may be used. For the V_H region, a primer pair such as VH1BACK (5' – AGG T(C/G)(A/C) A(A/G)C TGC AG(C/G) AGT C(A/T)G G – 3') **(SEQ ID NO: 32)** and CH1B may be used. After amplification, the V_K and V_H fragments may then be gel-purified and cloned into a cloning vector such as the TA cloning vector (Invitrogen) for sequence analyses by the dideoxytermination method. Sequences confirmed to be of immunoglobulin origin may then be used to construct chimeric Ab expression vectors using methods described by Leung *et al.* (Hybridoma, 13:469 (1994)).

Please delete paragraph [0138] on and replace it with the following paragraph:

[00138] Screening of the cDNA library may be accomplished by hybridization with labeled probes specific for the heavy and light chains. For example [^{32}P]-labeled probes such as MUCH-1 (5' – AGA CTG CAG GAG AGC TGG GAA GGT GTG CAC – 3') **(SEQ ID NO: 33)** for heavy chain and MUCK-1 (5' – GAA GCA CAC GAC TGA GGC ACC TCC AGA TGT – 3') **(SEQ ID NO: 34)** for light chain. Clones that are positive on a first screening may be transferred to duplicate plates and screened a second time with the same probes.

Please delete paragraph [0159] on and replace it with the following paragraph:

[00159] To obtain high-affinity scFv, an scFv library with a large repertoire can be constructed by isolating V-genes from non-immunized human donors using PCR primers corresponding to all known V_H, V_κ and V_λ gene families. See, e.g., Vaughn *et al.*, *Nat. Biotechnol.*, 14: 309-314 (1996). Following amplification, the V_κ and V_λ pools are combined to form one pool. These fragments are ligated into a phagemid vector. The scFv linker, (Gly-Gly-Gly-Gly- Ser)$_3$, **(SEQ ID NO: 35)** is then ligated into the phagemid upstream of the V_L fragment. The V_H and linker-V_L fragments are amplified and assembled on the J_H region. The resulting V_H-linker-V_L fragments are ligated into a phagemid vector. The phagemid library can be panned using filters, as described above, or using immunotubes (Nunc; Maxisorp). Similar results can be achieved by constructing a combinatorial immunoglobulin library from lymphocytes or spleen cells of immunized rabbits and by expressing the scFv constructs in *P. pastoris*. See, e.g., Ridder *et al.*, *Biotechnology*, 13: 255-260 (1995). Additionally, following isolation of an appropriate scFv, antibody fragments with higher binding affinities and slower dissociation rates can be obtained through affinity maturation processes such as CDR3 mutagenesis and chain shuffling. See, e.g., Jackson *et al.*, *Br. J. Cancer*, 78: 181-188 (1998); Osbourn *et al.*, *Immunotechnology*, 2: 181-196 (1996).

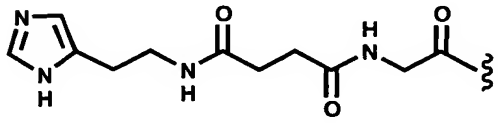
Please delete paragraph [0173] on and replace it with the following paragraph:

[00173] The MN3 antibodies and fragments thereof of the present invention can also be used to prepare functional bispecific single-chain antibodies (bscAb), also called diabodies, and can be produced in mammalian cells using recombinant methods. See, e.g., Mack *et al.*, *Proc. Natl. Acad. Sci.*, 92: 7021-7025, 1995, incorporated. For example, bscAb are produced by joining two single-chain Fv fragments via a glycine-serine linker using recombinant methods. The V light-chain (V_L) and V heavy-chain (V_H) domains of two antibodies of interest are isolated using standard PCR methods. The V_L and V_H cDNA's obtained from each hybridoma are then joined to form a single-chain fragment in a two-step fusion PCR. The first PCR step introduces the $(Gly_4\text{-}Ser_1)_3$ linker **(SEQ ID NO: 35)**, and the second step joins the V_L and V_H amplicons. Each single chain molecule is then cloned into a bacterial expression vector. Following amplification, one of the single-chain molecules is excised and sub-cloned into the other vector, containing the second single-chain molecule of interest. The resulting bscAb fragment is subcloned into an eukaryotic expression vector. Functional protein expression can be obtained by transfecting the vector into chinese hamster ovary cells. Bispecific fusion proteins are prepared in a similar manner. Bispecific single-chain antibodies and bispecific fusion proteins are included within the scope of the present invention.

Please delete paragraph [0195] on and replace it with the following paragraph:

[00195] Peptides having as few as two amino-acid residues may be used, preferably two to ten residues, if also coupled to other moieties such as chelating agents. The linker should be a low molecular weight conjugate, preferably having a molecular weight of less than 50,000 daltons, and advantageously less than about 20,000 daltons, 10,000 daltons or 5,000 daltons, including the metal ions in the chelates. For instance, the known peptide DTPA-Tyr-Lys(DTPA)-OH (wherein DTPA is diethylenetriaminepentaacetic acid) has been

used to generate antibodies against the indium-DTPA portion of the molecule. However, by use of the non-indium-containing molecule, and appropriate screening steps, new Abs against the tyrosyl-lysine dipeptide can be made. More usually, the antigenic peptide will have four or more residues, such as the peptide DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2 **(SEQ ID NO: 7)**, wherein DOTA is 1,4,7,10-tetraazacyclododecanetetraacetic acid and HSG is the histamine succinyl glycyl group of the formula:



Please delete paragraph [0196] on and replace it with the following paragraph:

[00196] The non-metal-containing peptide may be used as an immunogen, with resultant Abs screened for reactivity against the Phe-Lys-Tyr-Lys **(SEQ ID NO: 36)** backbone.

Please delete paragraph [0204] on and replace it with the following paragraph:

[00204] Chelators such as those disclosed in U.S. Patent 5,753,206, especially thiosemi-carbazonylglyoxylcysteine (Tscg-Cys) and thiosemicarbazinyl-acetylcysteine (Tsca-Cys) chelators are advantageously used to bind soft acid cations of Tc, Re, Bi and other transition metals, lanthanides and actinides that are tightly bound to soft base ligands, especially sulfur- or phosphorus-containing ligands. It can be useful to link more than one type of chelator to a peptide, e.g., a DTPA or similar chelator for, say In(III) cations, and a

thiol-containing chelator, e.g., Tscg-Cys, for Tc cations. Because antibodies to a di-DTPA hapten are known (Barbet '395, *supra*) and are readily coupled to a targeting antibody to form a bsAb, it is possible to use a peptide hapten with cold di-DTPA chelator and another chelator for binding a radioisotope, in a pretargeting protocol, for targeting the radioisotope. One example of such a peptide is Ac-Lys(DTPA)-Tyr-Lys(DTPA)-Lys(Tscg-Cys-)-NH_2 **(SEQ ID NO: 37)**. This peptide can be preloaded with In(III) and then labeled with 99-m-Tc cations, the In(III) ions being preferentially chelated by the DTPA and the Tc cations binding preferentially to the thiol-containing Tscg-Cys. Other hard acid chelators such as NOTA, DOTA, TETA and the like can be substituted for the DTPA groups, and Mabs specific to them can be produced using analogous techniques to those used to generate the anti-di-DTPA Mab.

Please delete paragraph [0206] on and replace it with the following paragraph:

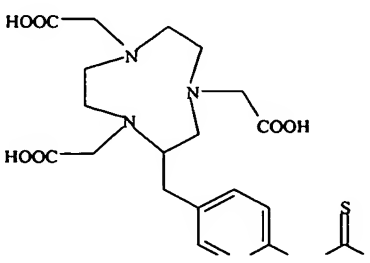
[00206] Preferred chelators include NOTA, DOTA and Tscg and combinations thereof. These chelators have been incorporated into a chelator-peptide conjugate motif as exemplified as described herein, such as in the following constructs:

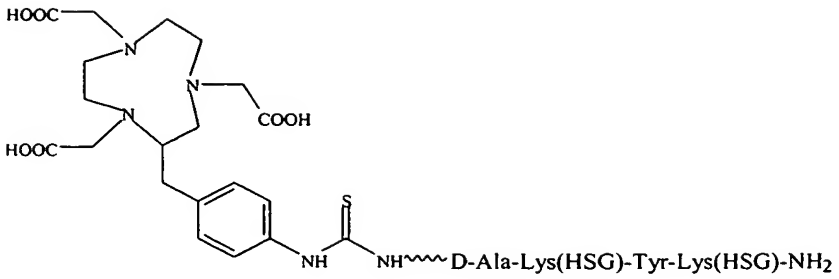
(a) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2;

(b) DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2 **(SEQ ID NO: 7)**;

(c) Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH_2;

(d)





and

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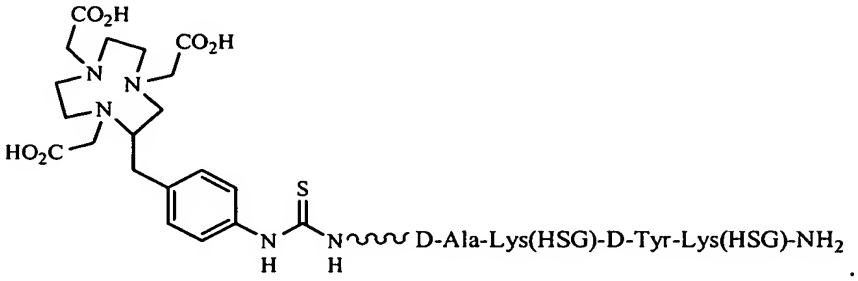


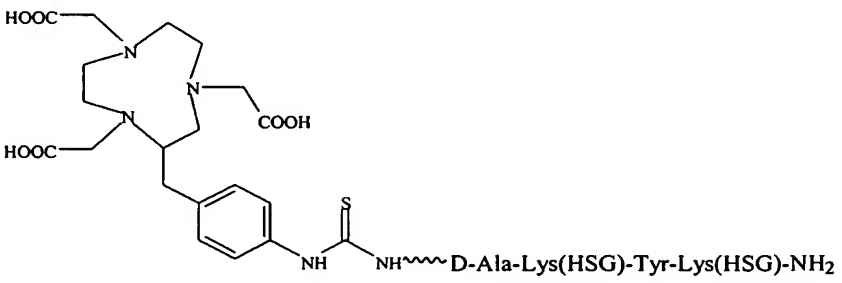
Please delete paragraph [0208] on and replace it with the following paragraph:

[00208] Chelators are coupled to the linker moieties using standard chemistries which are discussed more fully in the working Examples below. Briefly, the synthesis of the peptide Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys-)-NH_2 was accomplished by first attaching Aloc-Lys(Fmoc)-OH to a Rink amide resin on the peptide synthesizer. The protecting group abbreviations "Aloc" and "Fmoc" used herein refer to the groups allyloxycarbonyl and fluorenylmethyloxy carbonyl. The Fmoc-Cys(Trt)-OH and TscG were then added to the side chain of the lysine using standard Fmoc automated synthesis protocols to form the following peptide: Aloc-Lys(Tscg-Cys(Trt)-rink resin. The Aloc group was then removed. The peptide synthesis was then continued on the synthesizer to make the following peptide: (Lys(Aloc)-D-Tyr-Lys(Aloc)-Lys(Tscg-Cys(Trt)-)-rink resin. Following N-terminus acylation, and removal of the side chain Aloc protecting groups. The resulting

peptide was then treated with activated N-trityl-HSG-OH until the resin gave a negative test for amines using the Kaiser test. *See* Karacay *et al. Bioconjugate Chem. 11*:842-854 (2000). The synthesis of Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys-)-NH_2, as well as the syntheses of DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2; and DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2 **(SEQ ID NO: 7)** are described in greater detail below.

Please delete paragraph [0230] on and replace it with the following paragraph:

[00230] In a related vein, a method for detecting or treating neoplasms expressing an antigen recognized by MN3 in a mammal is described. This method comprises (A) administering an effective amount of a bispecific antibody or antibody fragment comprising at least one arm that specifically binds a targeted tissue and at least one other arm that specifically binds a targetable conjugate, wherein said one arm that specifically binds a targeted tissue is an MN3 antibody or fragment thereof; and (B) administering a targetable conjugate selected from the group consisting of (i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2; (ii) DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2 **(SEQ ID NO: 7)**; (iii) Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH_2;

(iv) 

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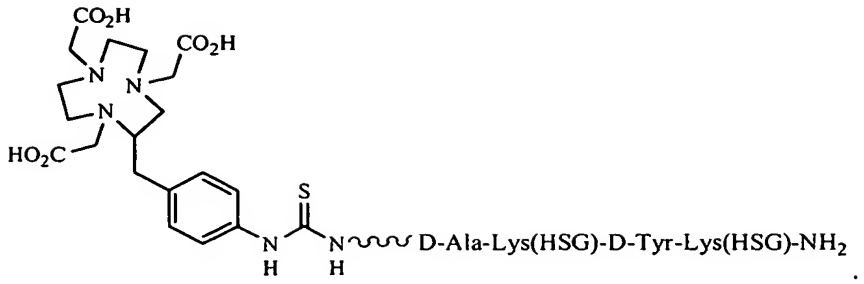
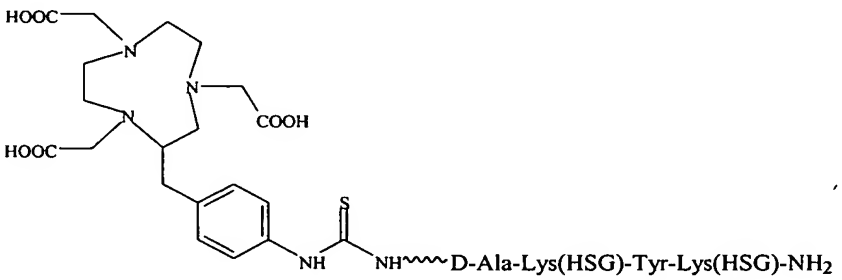
(v) 

Please delete paragraph [0239] on and replace it with the following paragraph:

[00239] Also contemplated herein is a kit useful for treating or identifying diseased tissues in a subject comprising: (A) a bi-specific antibody or antibody fragment having at least one arm that specifically binds a targeted tissue and at least one other arm that specifically binds a targetable conjugate, wherein said one arm that specifically binds a targeted tissue is an MN3 antibody or fragment thereof; (B) a first targetable conjugate which comprises a carrier portion which comprises or bears at least one epitope recognizable by said at least one other arm of said bi-specific antibody or antibody fragment, and one or more conjugated therapeutic or diagnostic agents; and (C) optionally, a clearing composition useful for clearing non-localized antibodies and antibody fragments; and (D) optionally, when said therapeutic agent conjugated to said first targetable conjugate is an enzyme, 1) a prodrug, when said enzyme is capable of converting said prodrug to a drug at the target site; or 2) a drug which is capable of being detoxified in said subject to form an intermediate of lower toxicity, when said enzyme is capable of reconverting said detoxified intermediate to a toxic form, and, therefore, of increasing the toxicity of said drug at the target site, or 3) a prodrug which is activated in said subject through natural processes and

is subject to detoxification by conversion to an intermediate of lower toxicity, when said enzyme is capable of reconverting said detoxified intermediate to a toxic form, and, therefore, of increasing the toxicity of said drug at the target site, or 4) a second targetable conjugate which comprises a carrier portion which comprises or bears at least one epitope recognizable by said at least one other arm of said bi-specific antibody or antibody fragment, and a prodrug, when said enzyme is capable of converting said prodrug to a drug at the target site. Preferably, the targetable conjugate is selected from the group consisting of (i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2; (ii) DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2 **(SEQ ID NO: 7)**; (iii) Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH_2;

(iv) 

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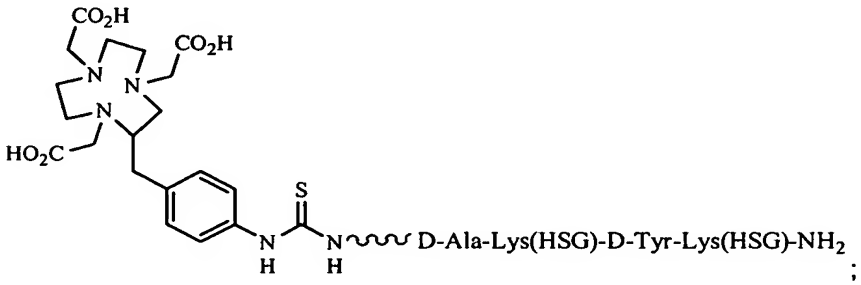
(v) 

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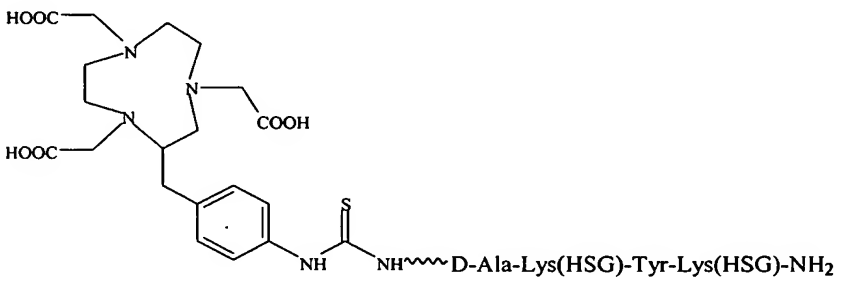
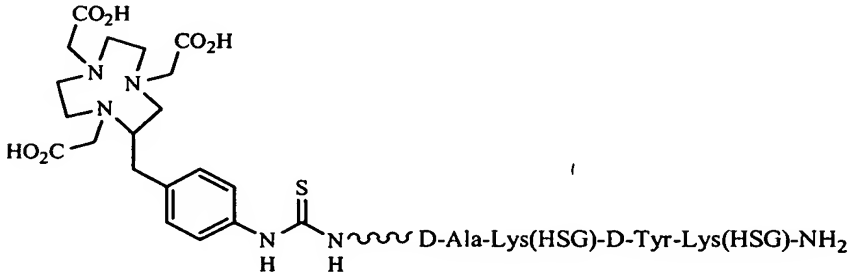
Please delete paragraph [0241] on and replace it with the following paragraph:

[00241] The present invention further provides a method for imaging malignant tissue or cells in a mammal expressing an antigen recognized by MN3; a method of

intraoperatively identifying/disclosing diseased tissues expressing an antigen recognized by MN3, in a subject; a method for endoscopic identification of diseased tissues expressing an antigen recognized by MN3, in a subject and a method for the intravascular identification of diseased tissues expressing an antigen recognized by MN3, in a subject. Such methods comprise (A) administering an effective amount of a bispecific antibody or antibody fragment comprising at least one arm that specifically binds a targeted tissue expressing an antigen recognized by MN3 and at least one other arm that specifically binds a targetable conjugate, wherein said one arm that specifically binds a targeted tissue is an MN3 antibody or fragment thereof; and (B) administering a targetable conjugate selected from the group consisting of (i) DOTA-Phe-Lys(HSG)-D-Tyr-Lys(HSG)-NH_2; (ii) DOTA-Phe-Lys(HSG)-Tyr-Lys(HSG)-NH_2 **(SEQ ID NO: 7)**; (iii) Ac-Lys(HSG)D-Tyr-Lys(HSG)-Lys(Tscg-Cys)-NH_2;

(iv) 

; and

(v) 

Please delete paragraph [0258] on and replace it with the following paragraph:

[00258] Each humanized variable chain was constructed in two parts, a 5'- and a 3'-half, designated as "A" and "B", respectively. Each half was produced by PCR amplification of a single stranded long synthetic oligonucleotide template with two short flanking primers using Taq polymerase. The amplified fragments were first cloned into the pCR4 TA cloning vector from Invitrogen and subjected to DNA sequencing. The templates and primer pairs are listed as follows:

Template	Primers	Product
Olgo G	Oligo 13/Oligo 14	VHA
Oligo H	Oligo 15/Oligo 16	VHB
Oligo I	Oligo 17/Oligo 18	VKA
Oligo J	Oligo 19/Oligo 20	VKB

The sequence information for the above identified oligonucleotides is as follows:

Oligo G (represents the minus strand of hMN3VH domain complementary to nt 25-173, 149 bp)
(SEQ ID NO: 38)

5'- GGCTCACCGG TGTAGGTGTT TATCCAGCCC ATCCACTCTA AACCCTGTCC
TGGAGCCTGT CTCACCCAGT TCATTCCATA GTTTCTGAAG GTATACCCAG
AAGCCTTGCA GGAGACCTTG ACGCTAGATC CAGGCTTCTT GACCTCAGC-3'

Oligo H (represents the minus strand of hMN3VH domain complementary to nt 181-329, 149 bp)
(SEQ ID NO: 39)

5'- TCGAGGCTAC TACCGTTGAA ATCCATCCAT CCCTTTCTTG CACAGAAATA
GAAAGCCGTG TCCTCAGATC TCAAGCTAGA CAGCTCCATA TAGGCAGTGT
TGGTAGATTC GTCGGCTGTG AAGGCAAACC GTCCCTTGAA GTCATCAGC-3'

Oligo 13 **(SEQ ID NO: 40)**

5'- CCAACTGCAG CAGTCTGGAG CTGAGGTCAA GAAGCCT-3'

Oligo 14 **(SEQ ID NO: 41)**

5'- GGCTCACCGG TGTAGGTGTT-3'

Oligo 15 **(SEQ ID NO: 42)**

5'-ACCTACACCG GTGAGCCAAC ATATGCTGAT GACTTCAAGG GACG-3'

Oligo 16 **(SEQ ID NO: 43)**

5'- GGTGACCGGG GTCCCTTGGC CCCAGTAGTC GAGGCTACTA CCGTTGA-3'

Oligo I (represents the minus strand of hMN3Vk domain complementary to nt 31-170, 140 bp) **(SEQ ID NO: 44)**

5'-GAAACTTTGT AGATCAGCAG CTTTGGAGCC TTACCTGGCT TCTGCTGGTA CCATTCTAAA TAGGTGTTTC CATTACTATG TACAATGCTC TGACTGGATC TACAAGAGAT GGACACTCTG TCACCCACGC TGGCGCTCAG-3'

Oligo J (represents the minus strand of hMN3VH domain complementary to nt 191-321, 131 bp) **(SEQ ID NO: 45)**

5'- GGTCCCGCCG CCGAACGTCG GAGGAACATG TGAACCTTGA AAGCAGTAGT AGGTGGCGAT GTCCTCTGGC TGGAGGCTGC TGATGGTGAA GGTGAAGTCG GTACCGCTAC CGCTACCGCT GAATCTGTCT G -3'

Oligo 17 **(SEQ ID NO: 46)**

5'-CAGCTGACCC AGAGCCCAAG CAGCCTGAGC GCCAGCGTGG G-3'

Oligo 18 **(SEQ ID NO: 47)**

5'-CTGGCACTCC GGAAAATCGG TTGGAAACTT TGTAGATCAG CAG-3'

Oligo 19 **(SEQ ID NO: 48)**

5'-CAACCGATTT TCCGGAGTGC CAGACAGATT CAGCGGT-3'

Oligo 20 **(SEQ ID NO: 49)**

5'-GATCTCCACC TTGGTCCCGC CGCCGAACGT CGG-3'

Please delete paragraph [0260] on and replace it with the following paragraph:

[00260] The same construction method as done for V_K was carried out VH with the following modifications. The 5'-end restriction site of the A fragments was PstI (CTGCAG) and the 3'-end restriction site of B fragments was BstEII (GGTCACC). These fragments were joined together upon ligation into the VHpBS2 vector at a common AgeI site (ACCGGT), resulting in full-length VH sequences (Figure 5B), which were confirmed by DNA sequencing. The assembled VH genes were subcloned as XhoI-BamHI restriction fragments into the expression vector containing the V_K sequence, hMN3VkpdHL2, predigested with XhoI and HindIII. To ligate the BamHI end od the VH fragment to the HindIII end of the vector, a linker, designated as HNB was used. The resulting expression vectors were designated as hMN3pdHL2.

HNB linker 5'-AGCTTGCGGCCGC-3' **(SEQ ID NO: 50)**

3'-ACGCCGGCGCTAG-5' **(SEQ ID NO: 51)**